



OIIPE

RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,794

TIME: 14:53:41

Input Set : A:\527c2.app

Output Set: N:\CRF3\02152002\J056794.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

C--> 6 (i) APPLICANT: Graves, Scott S.
7 Reno, John M.
8 Mallett, Robert W.
9 Hylarides, Mark D.
10 Searle, Stephen M.J.
11 Henry, Andrew H.
12 Pedersen, Jan T.
13 Rees, Anthony R.

15 (ii) TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
16 ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
17 PRETARGETING METHODS

19 (iii) NUMBER OF SEQUENCES: 19

21 (iv) CORRESPONDENCE ADDRESS:
22 (A) ADDRESSEE: Seed IP Law Group
23 (B) STREET: 701 Fifth Avenue, Suite 6300
24 (C) CITY: Seattle
25 (D) STATE: Washington
26 (E) COUNTRY: USA
27 (F) ZIP: 98104

29 (v) COMPUTER READABLE FORM:
30 (A) MEDIUM TYPE: Floppy disk
31 (B) COMPUTER: IBM PC compatible
32 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
33 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

35 (vi) CURRENT APPLICATION DATA:
C--> 36 (A) APPLICATION NUMBER: US/10/056,794
C--> 37 (B) FILING DATE: 24-Jan-2002
38 (C) CLASSIFICATION:

40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: Sharkey Ph.D., Richard G.
42 (B) REGISTRATION NUMBER: 32,629
43 (C) REFERENCE/DOCKET NUMBER: 690022.527C2

45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: (206) 622-4900
47 (B) TELEFAX: (206) 682-6031

50 (2) INFORMATION FOR SEQ ID NO: 1:
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 31 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear

ENTERED

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62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 CCTGACGAAT TCGTTGACAT TGATTATTGA C                               31
66 (2) INFORMATION FOR SEQ ID NO: 2:
68      (i) SEQUENCE CHARACTERISTICS:
69          (A) LENGTH: 32 base pairs
70          (B) TYPE: nucleic acid
71          (C) STRANDEDNESS: single
72          (D) TOPOLOGY: linear
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 CCTGACGCGG CCGCTTCGAT AAGCCAGTAA GC                               32
82 (2) INFORMATION FOR SEQ ID NO: 3:
84      (i) SEQUENCE CHARACTERISTICS:
85          (A) LENGTH: 44 base pairs
86          (B) TYPE: nucleic acid
87          (C) STRANDEDNESS: single
88          (D) TOPOLOGY: linear
94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
96 GTTCGGCTCG AGCACAGCTA GCATTATCTG GGATAAGCAT GCTG               44
98 (2) INFORMATION FOR SEQ ID NO: 4:
100     (i) SEQUENCE CHARACTERISTICS:
101         (A) LENGTH: 34 base pairs
102         (B) TYPE: nucleic acid
103         (C) STRANDEDNESS: single
104         (D) TOPOLOGY: linear
110     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
112 GTTACGGGGC CCCTAACACT CTCCCCTGTT GAAG                           34
114 (2) INFORMATION FOR SEQ ID NO: 5:
116     (i) SEQUENCE CHARACTERISTICS:
117         (A) LENGTH: 28 base pairs
118         (B) TYPE: nucleic acid
119         (C) STRANDEDNESS: single
120         (D) TOPOLOGY: linear
126     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
128 GTACGCGGAT CCCAGACACT GGACGCTG                                   28
130 (2) INFORMATION FOR SEQ ID NO: 6:
132     (i) SEQUENCE CHARACTERISTICS:
133         (A) LENGTH: 30 base pairs
134         (B) TYPE: nucleic acid
135         (C) STRANDEDNESS: single
136         (D) TOPOLOGY: linear
142     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
144 CATTCGGAAT TCGAACCATC ACAGTCTCGC                               30
146 (2) INFORMATION FOR SEQ ID NO: 7:
148     (i) SEQUENCE CHARACTERISTICS:
149         (A) LENGTH: 34 base pairs
150         (B) TYPE: nucleic acid
151         (C) STRANDEDNESS: single
152         (D) TOPOLOGY: linear
158     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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160	GCTGACGAAT TCTCATTTAC CCGGAGACAG GGAG	34
162	(2) INFORMATION FOR SEQ ID NO: 8:	
164	(i) SEQUENCE CHARACTERISTICS:	
165	(A) LENGTH: 26 base pairs	
166	(B) TYPE: nucleic acid	
167	(C) STRANDEDNESS: single	
168	(D) TOPOLOGY: linear	
174	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
176	CCGTCTATTA CTGTTCTAGA GAGGTC	26
178	(2) INFORMATION FOR SEQ ID NO: 9:	
180	(i) SEQUENCE CHARACTERISTICS:	
181	(A) LENGTH: 41 base pairs	
182	(B) TYPE: nucleic acid	
183	(C) STRANDEDNESS: single	
184	(D) TOPOLOGY: linear	
190	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
192	CAGCGTGCGG CCGCACCATG GACATCAGGG CTCCTGCTCA G	41
194	(2) INFORMATION FOR SEQ ID NO: 10:	
196	(i) SEQUENCE CHARACTERISTICS:	
197	(A) LENGTH: 26 base pairs	
198	(B) TYPE: nucleic acid	
199	(C) STRANDEDNESS: single	
200	(D) TOPOLOGY: linear	
206	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
208	AGCAGTACCA AAGCACGTAC CGGGTG	26
210	(2) INFORMATION FOR SEQ ID NO: 11:	
212	(i) SEQUENCE CHARACTERISTICS:	
213	(A) LENGTH: 23 base pairs	
214	(B) TYPE: nucleic acid	
215	(C) STRANDEDNESS: single	
216	(D) TOPOLOGY: linear	
222	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
224	TACGTGCTTT GGTACTGCTC CTC	23
226	(2) INFORMATION FOR SEQ ID NO: 12:	
228	(i) SEQUENCE CHARACTERISTICS:	
229	(A) LENGTH: 34 base pairs	
230	(B) TYPE: nucleic acid	
231	(C) STRANDEDNESS: single	
232	(D) TOPOLOGY: linear	
238	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
240	GCTGACGGAT CTCATTTAC CCGGAGACAG GGAG	34
242	(2) INFORMATION FOR SEQ ID NO: 13:	
244	(i) SEQUENCE CHARACTERISTICS:	
245	(A) LENGTH: 26 base pairs	
246	(B) TYPE: nucleic acid	
247	(C) STRANDEDNESS: single	
248	(D) TOPOLOGY: linear	
254	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
256	CCGTCTATTA CTGTTCTAGA GAGGTC	26

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258 (2) INFORMATION FOR SEQ ID NO: 14:

260 (i) SEQUENCE CHARACTERISTICS:

261 (A) LENGTH: 360 base pairs

262 (B) TYPE: nucleic acid

263 (C) STRANDEDNESS: single

264 (D) TOPOLOGY: linear

268 (ix) FEATURE:

269 (A) NAME/KEY: CDS

270 (B) LOCATION: 1..360

273 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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275 GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC      48
276 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
277   1           5           10           15
279 TCA GTC AGG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC      96
280 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
281           20           25           30
283 TAT ATG CAC TGG GTG ATA GAG AGG CCT GAA CAG GGC CTG GAG TGG ATT      144
284 Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile
285           35           40           45
287 GGA AGG ATT GAT CCT GCG AAT GGT AAT ACT AAA TGT GAC CCG AAG TTC      192
288 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe
289           50           55           60
291 CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC ACA GCC TAC      240
292 Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
293           65           70           75           80
295 CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAT TAC TGT      288
296 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
297           85           90           95
299 TCT AGA GAG GTC CTA ACT GGG ACG TGG TCT TTG GAC TAC TGG GGT CAA      336
300 Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln
301           100          105          110
303 GGA ACC TCA GTC ACC GTC TCC TCA      360
304 Gly Thr Ser Val Thr Val Ser Ser
305           115          120

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308 (2) INFORMATION FOR SEQ ID NO: 15:

310 (i) SEQUENCE CHARACTERISTICS:

311 (A) LENGTH: 120 amino acids

312 (B) TYPE: amino acid

313 (D) TOPOLOGY: linear

315 (ii) MOLECULE TYPE: protein

317 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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319 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
320   1           5           10           15
322 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
323           20           25           30
325 Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile
326           35           40           45
328 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe
329           50           55           60

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331 Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
332 65 70 75 80
334 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
335 85 90 95
337 Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln
338 100 105 110
340 Gly Thr Ser Val Thr Val Ser Ser
341 115 120
344 (2) INFORMATION FOR SEQ ID NO: 16:
346 (i) SEQUENCE CHARACTERISTICS:
347 (A) LENGTH: 321 base pairs
348 (B) TYPE: nucleic acid
349 (C) STRANDEDNESS: single
350 (D) TOPOLOGY: linear
354 (ix) FEATURE:
355 (A) NAME/KEY: CDS
356 (B) LOCATION: 1..321
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
361 GAC ATC CAG ATG ATT CAG TCT CCA TCG TCC ATG TTT GCC TCT CTG GGA 48
362 Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly
363 1 5 10 15
365 GAC AGA GTC AGT CTC TCT TGT CGG GCT AGT CAG GGC ATT AGA GGT AAT 96
366 Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn
367 20 25 30
369 TTA GAC TGG TAT CAG CAG AAA CCA GGT GGA ACT ATT AAA CTC CTG ATC 144
370 Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gly Thr Ile Lys Leu Leu Ile
371 35 40 45
373 TAC TCC ACA TCC AAT TTA AAT TCT GGT GTC CCA TCA AGG TTC AGT GGC 192
374 Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
375 50 55 60
377 AGT GGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC AGC CTA GAC TCT 240
378 Ser Gly Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Asp Ser
379 65 70 75 80
381 GAA GAT TTT GCA GAC TAT TAC TGT CTA CAG CGT AAT GCG TAT CCG TAC 288
382 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Arg Asn Ala Tyr Pro Tyr
383 85 90 95
385 ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA 321
386 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
387 100 105
390 (2) INFORMATION FOR SEQ ID NO: 17:
392 (i) SEQUENCE CHARACTERISTICS:
393 (A) LENGTH: 107 amino acids
394 (B) TYPE: amino acid
395 (D) TOPOLOGY: linear
397 (ii) MOLECULE TYPE: protein
399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
401 Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly
402 1 5 10 15
404 Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn

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VERIFICATION SUMMARY

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TIME: 14:53:42

Input Set : A:\527c2.app

Output Set: N:\CRF3\02152002\J056794.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]

L:36 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:37 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]